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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Bazan, J. Fernando
- (ii) TITLE OF INVENTION: MAMMALIAN CYTOKINE; RELATED REAGENTS
- (iii) NUMBER OF SEQUENCES: 16
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: DNAX Research Institute
  - (B) STREET: 901 California Avenue
  - (C) CITY: Palo Alto
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: US
  - (B) FILING DATE: 24-JUL-1998
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
- (A) APPLICATION NUMBER: US 60/053,765
  - (B) FILING DATE: 25-JUL-1997
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: Ching, Edwin P.
  - (B) REGISTRATION NUMBER: 34,090
  - (C) REFERENCE/DOCKET NUMBER: DX0758K1
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: (650)852-9196
  - (B) TELEFAX: (650)496-1200

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 570 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
  - (B) LOCATION: 1..567

Sequence Listing filed in USSN 09/122,443  
For Reissue Application for Patent 6,060,284

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 64..567

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG CTG GGG AGC AGA GCT GTA ATG CTG CTG TTG CTG CTG CCC TGG ACA	48
Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr	
-21 -20 -15 -10	
GCT CAG GGC AGA GCT GTG CCT GGG GGC AGC AGC CCT GCC TGG ACT CAG	96
Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln	
-5 1 5 10	
TGC CAG CAG CTT TCA CAG AAG CTC TGC ACA CTG GCC TGG AGT GCA CAT	144
Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His	
15 20 25	
CCA CTA GTG GGA CAC ATG GAT CTA AGA GAA GAG GGA GAT GAA GAG ACT	192
Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr	
30 35 40	
ACA AAT GAT GTT CCC CAT ATC CAG TGT GGA GAT GGC TGT GAC CCC CAA	240
Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln	
45 50 55	
GGA CTC AGG GAC AAC AGT CAG TTC TGC TTG CAA AGG ATC CAC CAG GGT	288
Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly	
60 65 70 75	
CTG ATT TTT TAT GAG AAG CTG CTA GGA TCG GAT ATT TTC ACA GGG GAG	336
Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu	
80 85 90	
CCT TCT CTG CTC CCT GAT AGC CCT GTG GCG CAG CTT CAT GCC TCC CTA	384
Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu	
95 100 105	
CTG GGC CTC AGC CAA CTC CTG CAG CCT GAG GGT CAC CAC TGG GAG ACT	432
Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr	
110 115 120	
CAG CAG ATT CCA AGC CTC AGT CCC AGC CAG CCA TGG CAG CGT CTC CTT	480
Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu	
125 130 135	
CTC CGC TTC AAA ATC CTT CGC AGC CTC CAG GCC TTT GTG GCT GTA GCC	528
Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala	
140 145 150 155	
GCC CGG GTC TTT GCC CAT GGA GCA GCA ACC CTG AGT CCC TAA	570
Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro	
160 165	

(2) INFORMATION FOR SEQ ID NO:2:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

Met Leu Gly Ser Arg Ala Val Met Leu Leu Leu Leu Leu Pro Trp Thr  
-21 -20 -15 -10

Ala Gln Gly Arg Ala Val Pro Gly Gly Ser Ser Pro Ala Trp Thr Gln  
-5                      1                      5                      10

Cys Gln Gln Leu Ser Gln Lys Leu Cys Thr Leu Ala Trp Ser Ala His  
15 20 25

Pro Leu Val Gly His Met Asp Leu Arg Glu Glu Gly Asp Glu Glu Thr  
30 35 40

Thr Asn Asp Val Pro His Ile Gln Cys Gly Asp Gly Cys Asp Pro Gln  
45 50 55

Gly Leu Arg Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile His Gln Gly  
60 65 70 75

Leu Ile Phe Tyr Glu Lys Leu Leu Gly Ser Asp Ile Phe Thr Gly Glu  
80 85 90

Pro Ser Leu Leu Pro Asp Ser Pro Val Ala Gln Leu His Ala Ser Leu  
95 100 105

Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Gly His His Trp Glu Thr  
110 115 120

Gln Gln Ile Pro Ser Leu Ser Pro Ser Gln Pro Trp Gln Arg Leu Leu  
125 130 135

Leu Arg Phe Lys Ile Leu Arg Ser Leu Gln Ala Phe Val Ala Val Ala  
140 145 150 155

Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Ser Pro  
160 165

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100

(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 176..700

CGCTTAGAAG TCGGACTACA GAGTTAGACT CAGAACCAAA GGAGGTGGAT AGGGGGTCCA	60
CAGGCCTGGT GCAGATCACA GAGCCAGCCA GATCTGAGAA GCAGGGAACA AG ATG Met -21	115
CTG GAT TGC AGA GCA GTA ATA ATG CTA TGG CTG TTG CCC TGG GTC ACT Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val Thr -20 -15 -10 -5	163
CAG GGC CTG GCT GTG CCT AGG AGT AGC AGT CCT GAC TGG GCT CAG TGC Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln Cys 1 5 10	211
CAG CAG CTC TCT CGG AAT CTC TGC ATG CTA GCC TGG AAC GCA CAT GCA Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His Ala 15 20 25	259
CCA GCG GGA CAT ATG AAT CTA CTA AGA GAA GAA GAG GAT GAA GAG ACT Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu Thr 30 35 40	307
AAA AAT AAT GTG CCC CGT ATC CAG TGT GAA GAT GGT TGT GAC CCA CAA Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro Gln 45 50 55 60	355
GGA CTC AAG GAC AAC AGC CAG TTC TGC TTG CAA AGG ATC CGC CAA GGT Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln Gly 65 70 75	403
CTG GCT TTT TAT AAG CAC CTG CTT GAC TCT GAC ATC TTC AAA GGG GAG Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly Glu 80 85 90	451
CCT GCT CTA CTC CCT GAT AGC CCC ATG GAG CAA CTT CAC ACC TCC CTA Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser Leu 95 100 105	499
CTA GGA CTC AGC CAA CTC CTC CAG CCA GAG GAT CAC CCC CGG GAG ACC Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu Thr 110 115 120	547
CAA CAG ATG CCC AGC CTG AGT TCT AGT CAG CAG TGG CAG CGC CCC CTT Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro Leu 125 130 135 140	595
CTC CGT TCC AAG ATC CTT CGA AGC CTC CAG GCC TTT TTG GCC ATA GCT Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile Ala	643

GCC CGG GTC	TTT GCC CAC GGA GCA GCA ACT CTG ACT GAG CCC TTA GTG	691
Ala Arg Val	Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu Val	
	160 165 170	
CCA ACA GCT	TAAGGATGCC CAGGTTCCCA TGGCTACCAT GATAAGACTA	740
Pro Thr Ala		
	175	
ATCTATCAGC	CCAGACATCT ACCAGTTAAT TAACCCATTA GGACTTGTGC TGTTCTTGTT	800
TCGTTTGT	TTT TGC GTGAAGG GCAAGGACAC CATTATTAAAGAGAAAAGAA ACAAACCCCA	860
GAGCAGGCAG	CTGGCTAGAG AAAGGAGCTG GAGAAGAAGA ATAAAGTCTC GAGCCCTTGG	920
CCTTGGAAGC	GGGCAAGCAG CTGCGTGGCC TGAGGGGAAG GGGGCGGTGG CATCGAGAAA	980
CTGTGAGAAA	ACCCAGAGCA TCAGAAAAAG TGAGCCCAGG CTTTGGCCAT TATCTGTAAG	1040
AAAAACAAGA	AAAGGGGAAC ATTATACTTT CCTGGGTGGC TCAGGGAAAT GTGCAGATGC	1100
ACAGTACTCC	AGACAGCAGC TCTGTACCTG CCTGCTCTGT CCCTCAGTTC TAACAGAATC	1160
TAGTCACTAA	GAAC TAACAG GACTACCAAT ACGAACTGAC AAA	1203

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Leu Asp Cys Arg Ala Val Ile Met Leu Trp Leu Leu Pro Trp Val  
-21 -20 -15 -10

Thr Gln Gly Leu Ala Val Pro Arg Ser Ser Ser Pro Asp Trp Ala Gln  
-5 1 5 10

Cys Gln Gln Leu Ser Arg Asn Leu Cys Met Leu Ala Trp Asn Ala His  
15 20 25

Ala Pro Ala Gly His Met Asn Leu Leu Arg Glu Glu Glu Asp Glu Glu  
30 35 40

Thr Lys Asn Asn Val Pro Arg Ile Gln Cys Glu Asp Gly Cys Asp Pro  
45 50 55

Gln Gly Leu Lys Asp Asn Ser Gln Phe Cys Leu Gln Arg Ile Arg Gln  
60 65 70 75

Gly Leu Ala Phe Tyr Lys His Leu Leu Asp Ser Asp Ile Phe Lys Gly  
80 85 90

[illegible]

Glu Pro Ala Leu Leu Pro Asp Ser Pro Met Glu Gln Leu His Thr Ser  
95 100 105

Leu Leu Gly Leu Ser Gln Leu Leu Gln Pro Glu Asp His Pro Arg Glu  
110 115 120

Thr Gln Gln Met Pro Ser Leu Ser Ser Ser Gln Gln Trp Gln Arg Pro  
125 130 135

Leu Leu Arg Ser Lys Ile Leu Arg Ser Leu Gln Ala Phe Leu Ala Ile  
140 145 150 155

Ala Ala Arg Val Phe Ala His Gly Ala Ala Thr Leu Thr Glu Pro Leu  
160 165 170

Val Pro Thr Ala  
175

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Ser Cys Leu Gln Arg Ile His Gln Gly Leu Val Phe Tyr Glu Lys Leu  
1 5 10 15

Leu Gly Ser Asp Ile Phe Thr Gly Glu Pro Ser Leu His Pro Asp Gly  
20 25 30

Ser Val Gly Gln Leu His Ala Ser Leu Leu Gly Leu Arg Gln Leu Leu  
35 40 45

Gln Pro Glu Gly His His Trp Glu Thr Glu Gln Thr Pro Ser Pro Ser  
50 55 60

Pro Ser Gln Pro Trp Gln Arg Leu Leu Leu Arg Leu Lys Ile Leu Arg  
65 70 75 80

Ser Leu Gln Ala Phe Val Ala Val Ala Ala Arg Val Phe Ala His Gly  
85 90 95

Ala Ala Thr Leu Ser Gln  
100

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Thr	Pro	Leu	Gly	Pro	Ala	Arg	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	1	5	10	15
Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Ala	Asp	Gly	Ala	Glu	Leu	Gln	20	25	30	
Glu	Arg	Leu	Cys	Ala	Ala	His	Lys	Leu	Cys	His	Pro	Glu	Glu	Leu	Met	35	40	45	
Leu	Leu	Arg	His	Ser	Leu	Gly	Ile	Pro	Gln	Ala	Pro	Leu	Ser	Ser	Cys	50	55	60	
Ser	Ser	Gln	Ser	Leu	Gln	Leu	Arg	Gly	Cys	Leu	Asn	Gln	Leu	His	Gly	65	70	75	80
Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	Leu	Ala	Gly	Ile	Ser	85	90	95	
Pro	Glu	Leu	Ala	Pro	Thr	Leu	Asp	Thr	Leu	Gln	Leu	Asp	Val	Thr	Asp	100	105	110	
Phe	Ala	Thr	Asn	Ile	Trp	Leu	Gln	Met	Glu	Asp	Leu	Gly	Ala	Ala	Pro	115	120	125	
Ala	Val	Gln	Pro	Thr	Gln	Gly	Ala	Met	Pro	Thr	Phe	Thr	Ser	Ala	Phe	130	135	140	
Gln	Arg	Arg	Ala	Gly	Gly	Val	Leu	Val	Ala	Ser	Gln	Leu	His	Arg	Phe	145	150	155	160
Leu	Glu	Leu	Ala	Tyr	Arg	Gly	Leu	Arg	Tyr	Leu	Ala	Glu	Pro	165	170				

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Thr Pro Leu Gly Pro Thr Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys  
1 5 10 15  
Cys Leu Glu Gln Val Arg Lys Val Gln Ala Asp Gly Thr Ala Leu Gln  
20 25 30  
Glu Arg Leu Cys Ala Ala His Lys Leu Cys His Pro Glu Glu Leu Val  
35 40 45  
Leu Leu Gly His Ala Leu Gly Ile Pro Gln Ala Pro Leu Ser Ser Cys  
50 55 60  
Ser Ser Gln Ala Leu Gln Leu Thr Gly Cys Leu Arg Gln Leu His Ser  
65 70 75 80  
Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Ala Gly Ile Ser  
85 90 95  
Pro Glu Leu Ala Pro Thr Leu Asp Met Leu Gln Leu Asp Ile Thr Asp  
100 105 110  
Phe Ala Ile Asn Ile Trp Gln Gln Met Glu Asp Val Gly Met Ala Pro  
115 120 125  
Ala Val Pro Pro Thr Gln Gly Thr Met Pro Thr Phe Thr Ser Ala Phe  
130 135 140  
Gln Arg Arg Ala Gly Gly Thr Leu Val Ala Ser Asn Leu Gln Ser Phe  
145 150 155 160  
Leu Glu Val Ala Tyr Arg Ala Leu Arg His Phe Thr Lys Pro  
165 170

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys  
1 5 10 15  
Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln  
20 25 30  
Glu Lys Leu Val Ser Glu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu  
35 40 45

Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu  
 50 55 60  
 Ser Ser Cys Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln  
 65 70 75 80  
 Leu His Ser Gly Leu Met Ala Pro Ala Leu Gln Pro Thr Gln Gly Ala  
 85 90 95  
 Met Pro Ala Phe Ala Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu  
 100 105 110  
 Val Ala Ser His Leu Gln Ser Phe Leu Glu Val Ser Tyr Arg Val Leu  
 115 120 125  
 Arg His Leu Ala Gln Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu  
 130 135 140  
 Gly Ile Ser Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp  
 145 150 155 160  
 Val Ala Asp Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly  
 165 170 175  
 Pro

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Val Pro Leu Val Thr Val Ser Ala Leu Pro Pro Ser Leu Pro Leu Pro  
 1 5 10 15  
 Arg Ser Phe Leu Leu Lys Ser Leu Glu Gln Val Arg Lys Ile Gln Ala  
 20 25 30  
 Ser Gly Ser Val Leu Leu Glu Gln Leu Cys Ala Thr Tyr Lys Leu Cys  
 35 40 45  
 His Pro Glu Glu Leu Val Leu Leu Gly His Ser Leu Gly Ile Pro Lys  
 50 55 60  
 Ala Ser Leu Ser Gly Cys Ser Ser Gln Ala Leu Gln Gln Thr Gln Cys  
 65 70 75 80

Leu Ser Gln Leu His Ser Gly Leu Cys Leu Tyr Gln Gly Leu Leu Gln  
85 90 95

Ala Leu Ser Gly Ile Ser Pro Ala Leu Ala Pro Thr Leu Asp Leu Leu  
100 105 110

Gln Leu Asp Val Ala Asn Phe Ala Thr Thr Ile Trp Gln Gln Met Glu  
115 120 125

Asn Leu Gly Val Ala Pro Thr Val Gln Pro Thr Gln Ser Ala Met Pro  
130 135 140

Ala Phe Thr Ser Ala Phe Gln Arg Arg Ala Gly Gly Val Leu Ala Ile  
145 150 155 160

Ser Tyr Leu Gln Gly Phe Leu Glu Thr Ala Arg Leu Ala Leu His His  
165 170 175

Leu Ala

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Phe Pro Thr Pro Gly Pro Leu Gly Gly Asp Ser Lys Asp Asp Ala  
1 5 10 15

Thr Ser Asn Arg Pro Pro Leu Thr Ser Ala Asp Lys Met Glu Asp Phe  
20 25 30

Ile Lys Phe Ile Leu Gly Lys Ile Ser Ala Leu Arg Asn Glu Met Cys  
35 40 45

Asp Lys Tyr Asn Lys Cys Glu Asp Ser Lys Glu Val Leu Ala Glu Asn  
50 55 60

Asn Leu Asn Leu Pro Lys Leu Ala Glu Lys Asp Arg Cys Phe Gln Ser  
65 70 75 80

Arg Phe Asn Gln Glu Thr Cys Leu Thr Arg Ile Thr Thr Gly Leu Gln  
85 90 95

Glu Phe Gln Ile His Leu Lys Tyr Leu Glu Ser Asn Tyr Glu Gly Asn  
100 105 110

Lys Asp Asn Ala His Ser Val Tyr Ile Ser Thr Lys His Leu Leu Gln

FOUO 930303

115

120

125

Thr Leu Arg Pro Met Asn Gln Ile Glu Val Thr Thr Pro Asp Pro Thr  
 130 135 140

Thr Asp Ala Ser Leu Gln Ala Leu Phe Lys Ser Gln Asp Lys Trp Leu  
 145 150 155 160

Lys His Thr Thr Ile His Leu Ile Leu Arg Arg Leu Glu Asp Phe Leu  
 165 170 175

Gln Phe Ser Leu Arg Ala Ile Arg Ile Met  
 180 185

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala Phe Pro Thr Pro Gly Pro Leu Gly Gly Asp Ala Thr Ser Asn Arg  
 1 5 10 15

Leu Pro Leu Thr Pro Ala Asp Lys Met Glu Glu Leu Ile Lys Tyr Ile  
 20 25 30

Leu Gly Lys Ile Ser Ala Leu Lys Lys Glu Met Cys Asp Asn Tyr Asn  
 35 40 45

Lys Cys Glu Asp Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu  
 50 55 60

Pro Lys Leu Ala Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Gln  
 65 70 75 80

Glu Thr Cys Leu Thr Arg Ile Thr Thr Gly Leu Gln Glu Phe Gln Ile  
 85 90 95

Tyr Leu Lys Phe Leu Gln Asp Lys Tyr Glu Gly Asp Lys Glu Asn Ala  
 100 105 110

Lys Ser Val Tyr Thr Ser Thr Asn Val Leu Leu Gln Met Leu Lys Arg  
 115 120 125

Lys Gly Lys Asn Gln Asp Glu Val Thr Ile Pro Val Pro Thr Val Glu  
 130 135 140

Val Gly Leu Gln Leu Ser Cys Ser His Arg Arg Val Ala Glu Ala His  
 145 150 155 160

102230 332300

Asn Asn His Leu Thr Leu Arg Arg Leu Glu Asp Phe Leu Gln Leu Arg  
165 170 175

(2) INFORMATION FOR SEQ ID NO:12:

- (A) LENGTH: 188 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile' Asp Lys Gln  
20 25 30

Ile Arg Tyr Ile Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys  
35 40 45

Asn Lys Ser Asn Met Cys Glu Ser Ser Lys Glu Ala Leu Ala Glu Asn  
50 55 60

Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly Cys Phe Gln Ser  
65 70 75 80

Gly Phe Asn Glu Glu Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu  
85 90 95

Glu Phe Glu Val Tyr Leu Glu Tyr Leu Gln Asn Arg Phe Glu Ser Ser  
100 105 110

Glu Glu Gln Ala Arg Ala Val Gln Met Ser Thr Lys Val Leu Ile Gln  
115 120 125

Phe Leu Gln Lys Lys Ala Lys Asn Leu Asp Ala Ile Thr Thr Pro Asp  
130 135 140

Pro Thr Thr Asn Ala Ser Leu Leu Thr Lys Leu Gln Ala Gln Asn Gln  
145 150 155 160

Trp Leu Gln Asp Met Thr Thr His Leu Ile Leu Arg Ser Phe Lys Glu  
165 170 175

Phe Leu Gln Ser Ser Leu Arg Ala Leu Arg Gln Met  
180 185

[illegible]

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Ala Phe Pro Thr Pro Gly Pro Leu Gly Glu Asp Phe Lys Asn Asp Thr  
1 5 10 15  
Thr Pro Ser Arg Leu Leu Leu Thr Thr Pro Glu Lys Thr Glu Ala Leu  
20 25 30  
Ile Lys His Ile Val Asp Lys Ile Ser Ala Ile Arg Lys Glu Ile Cys  
35 40 45  
Glu Lys Asn Asp Glu Cys Glu Asn Ser Lys Glu Thr Leu Ala Glu Asn  
50 55 60  
Lys Leu Lys Leu Pro Lys Met Glu Glu Lys Asp Gly Cys Phe Gln Ser  
65 70 75 80  
Gly Phe Asn Gln Ala Ile Cys Leu Ile Lys Thr Thr Ala Gly Leu Leu  
85 90 95  
Glu Tyr Gln Ile Tyr Leu Asp Phe Leu Gln Asn Glu Phe Glu Gly Asn  
100 105 110  
Gln Glu Thr Val Met Glu Leu Gln Ser Ser Ile Arg Thr Leu Ile Gln  
115 120 125  
Ile Leu Lys Glu Lys Ile Ala Gly Leu Ile Thr Thr Pro Ala Thr His  
130 135 140  
Thr Asp Met Leu Glu Lys Met Gln Ser Ser Asn Glu Trp Val Lys Asn  
145 150 155 160  
Ala Lys Val Ile Ile Ile Leu Arg Ser Leu Glu Asn Phe Leu Gln Phe  
165 170 175  
Ser Leu Arg Ala Ile Arg Met Lys  
180

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Phe Pro Thr Ser Gln Val Arg Arg Gly Asp Phe Thr Glu Asp Thr  
1 5 10 15  
Thr Pro Asn Arg Pro Val Tyr Thr Thr Ser Gln Val Gly Gly Leu Ile  
20 25 30  
Thr His Val Leu Trp Glu Ile Val Glu Met Arg Lys Glu Leu Cys Asn  
35 40 45  
Gly Asn Ser Asp Cys Met Asn Asn Asp Asp Ala Leu Ala Glu Asn Asn  
50 55 60  
Leu Lys Leu Pro Glu Ile Gln Arg Asn Asp Gly Cys Tyr Gln Thr Gly  
65 70 75 80  
Tyr Asn Gln Glu Ile Cys Leu Leu Lys Ile Ser Ser Gly Leu Leu Glu  
85 90 95  
Tyr His Ser Tyr Leu Glu Tyr Met Lys Asn Asn Leu Lys Asp Asn Lys  
100 105 110  
Lys Asp Lys Ala Arg Val Leu Gln Arg Asp Thr Glu Thr Leu Ile His  
115 120 125  
Ile Phe Asn Gln Glu Val Lys Asp Leu His Lys Ile Val Leu Pro Thr  
130 135 140  
Pro Ile Ser Asn Ala Leu Leu Thr Asp Lys Leu Glu Ser Gln Lys Glu  
145 150 155 160  
Trp Leu Arg Thr Lys Thr Ile Gln Phe Ile Leu Lys Ser Leu Glu Glu  
165 170 175  
Phe Leu Lys Val Thr Leu Arg Ser Thr Arg Gln Thr  
180 185

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:





[illegible]